

## SEQUENCE LISTING

<110> CHEN, WENFANG  
MEEK, THOMAS D.  
POWELL, DAVID J.  
TEW, DAVID G.

<120> Method of Site Specific Labeling of Proteins and Uses  
Therefor

<130> P50892

<140> 09/889,344

<141> 2001-07-16

<150> PCT/US00/01481

<151> 2000-01-20

<150> US 60/117,327

<151> 1999-01-22

<160> 16

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> unsure

<222> (5)

<223> Where Xaa at position (5) can represent Leucine or Isoleucine

<400> 1

Gln Ser Lys Val Xaa

1

5

<210> 2

<211> 207

<212> PRT

<213> Artificial Sequence

<220>

<221> unsure

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<223> Where Xaa can represent none or any one of the twenty naturally

<223> occurring amino acids

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20

25

30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

35

40

45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50

55

60

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65						70					75					80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
						85					90					95
Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Ser	Lys	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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						145					150					155
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						165					170					175
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
						180					185					190
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<211> 207

<212> PRT

<213> Artificial Sequence

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<221> unsure

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 <223> Where Xaa can represent none or any one of the twenty naturally  
 <223> occurring amino acids

<400> 3

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				20					25					30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				35					40					45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				50					55					60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65									70					75	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									85					90	
Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Ser	Lys	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									100					105	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									115					120	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									130					135	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145														150	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									165					170	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									180					185	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
									195					200	
														205	

<210> 4

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Derivative of a factor XIII substrate

<400> 4

Leu Ser Leu Ser Gln Ser Lys Val Leu Gly  
1 5 10

<210> 5

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Derivative of a factor XIII substrate

<400> 5

Ile Gly Glu Gly Gln Ser Lys Val Leu Gly  
1 5 10

<210> 6

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Derivative of a factor XIII substrate

<400> 6

Leu Gly Pro Gly Gln Ser Lys Val Ile Gly  
1 5 10

<210> 7

<211> 81

<212> DNA

<213> Unknown

<220>

<223> Oligonucleotide designed to introduce Q tag

<400> 7

tgtacctcag accatatgag cctgtccctg tcccagtcca aagttctgcc ggggtccgagc

actatcgaag aacgcgttaa g

81

<210> 8

<211> 37

<212> DNA

<213> Unknown

<220>

<223> Oligonucleotide designed to introduce Q tag

<400> 8

tgatgtcagt caagcttacg cctgggtggcc gttgatg

37

<210> 9

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Derivative of a factor XIII substrate

<400> 9

Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro

1

5

10

<210> 10

<211> 37

<212> DNA

<213> Unknown

<220>

<223> Oligonucleotide designed to introduce Q tag

<400> 10

tgtacctcag accatatgag cactatcgaa gaacgcg

37

<210> 11

<211> 78

<212> DNA

<213> Unknown

<223> Oligonucleotide designed to introduce Q tag

tgatgtcagt caagcttacg gacccggcag aactttggac tgggacaggg acagcgcctg 60  
gtggccgttg atgtaatc 78

<213> Artificial Sequence

<223> Derivative of E. coli ACP protein

Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro  
1 5 10

<213> Unknown

<223> Oligonucleotide designed to introduce Q tag into  
Streptococcus haemophilus FabH gene

tatcatatga gctgtccct gtcccagtc aaagtctgc cgggtccggg taccctcgag 60  
ggatccgctt ttgcaaaaat aagtcagggt gc 92

<213> Unknown

<223> Oligonucleotide designed to introduce Q tag into

Streptococcus haemophilus FabH gene

<400> 14

ctcagatctg agctcactag tggatcctta aattgtaaga atgagcgtgc ccc

53

<210> 15

<211> 364

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified sequence of Streptococcus haemophilus FabH

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Met	Gly	His	His	His	His	His	His	His	His	His	His	Ser	Ser	Gly	His
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Ile	Glu	Gly	Arg	His	Met	Ser	Leu	Ser	Leu	Ser	Gln	Ser	Lys	Val	Leu
			20					25					30		
Pro	Gly	Pro	Gly	Thr	Leu	Glu	Gly	Ser	Ala	Phe	Ala	Lys	Ile	Ser	Gln
			35				40					45			
Val	Ala	His	Tyr	Val	Pro	Glu	Gln	Val	Val	Thr	Asn	His	Asp	Leu	Ala
			50				55				60				
Gln	Ile	Met	Asp	Thr	Asn	Asp	Glu	Trp	Ile	Ser	Ser	Arg	Thr	Gly	Ile
65					70					75					80
Arg	Gln	Arg	His	Ile	Ser	Arg	Thr	Glu	Ser	Thr	Ser	Asp	Leu	Ala	Thr
				85						90					95
Glu	Val	Ala	Lys	Lys	Leu	Met	Ala	Lys	Ala	Gly	Ile	Thr	Gly	Lys	Glu
			100					105						110	
Leu	Asp	Phe	Ile	Ile	Leu	Ala	Thr	Ile	Thr	Pro	Asp	Ser	Met	Met	Pro
			115				120					125			
Ser	Thr	Ala	Ala	Arg	Val	Gln	Ala	Asn	Ile	Gly	Ala	Asn	Lys	Ala	Phe
			130				135					140			
Ala	Phe	Asp	Leu	Thr	Ala	Ala	Cys	Ser	Gly	Phe	Val	Phe	Ala	Leu	Ser
145					150					155					160
Thr	Ala	Glu	Lys	Phe	Ile	Ala	Ser	Gly	Arg	Phe	Gln	Lys	Gly	Leu	Val
				165					170					175	
Ile	Gly	Ser	Glu	Thr	Leu	Ser	Lys	Ala	Val	Asp	Trp	Ser	Asp	Arg	Ser
			180					185					190		
Thr	Ala	Val	Leu	Phe	Gly	Asp	Gly	Ala	Gly	Gly	Val	Leu	Leu	Glu	Ala
			195					200						205	



Ser Glu Gln Glu His Phe Leu Ala Glu Ser Leu Asn Ser Asp Gly Ser  
 210 215 220  
 Arg Ser Glu Cys Leu Thr Tyr Gly His Ser Gly Leu His Ser Pro Phe  
 225 230 235 240  
 Ser Asp Gln Glu Ser Ala Asp Ser Phe Leu Lys Met Asp Gly Arg Thr  
 245 250 255  
 Val Phe Asp Phe Ala Ile Arg Asp Val Ala Lys Ser Ile Lys Gln Thr  
 260 265 270  
 Ile Asp Glu Ser Pro Ile Glu Val Thr Asp Leu Asp Tyr Leu Leu Leu  
 275 280 285  
 His Gln Ala Asn Asp Arg Ile Leu Asp Lys Met Ala Arg Lys Ile Gly  
 290 295 300  
 Val Asp Arg Ala Lys Leu Pro Ala Asn Met Met Glu Tyr Gly Asn Thr  
 305 310 315 320  
 Ser Ala Ala Ser Ile Pro Ile Leu Leu Ser Glu Cys Val Glu Gln Gly  
 325 330 335  
 Leu Ile Pro Leu Asp Gly Ser Gln Thr Val Leu Leu Ser Gly Phe Gly  
 340 345 350  
 Gly Gly Leu Thr Trp Gly Thr Leu Ile Leu Thr Ile  
 355 360

<210> 16

<211> 503

<212> PRT

<213> Artificial Sequence

<220>

<223> Modified sequence of Erythropoietin receptor  
fusion protein

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Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys  
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 Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp  
 20 25 30  
 Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu  
 35 40 45  
 Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp  
 50 55 60

Glu	Glu	Ala	Ala	Ser	Ala	Gly	Val	Gly	Pro	Gly	Asn	Tyr	Ser	Phe	Ser	65	70	75	80
Tyr	Gln	Leu	Glu	Asp	Glu	Pro	Trp	Lys	Leu	Cys	Arg	Leu	His	Gln	Ala	85	90	95	
Pro	Thr	Ala	Arg	Gly	Ala	Val	Arg	Phe	Trp	Cys	Ser	Leu	Pro	Thr	Ala	100	105	110	
Asp	Thr	Ser	Ser	Phe	Val	Pro	Leu	Glu	Leu	Arg	Val	Thr	Ala	Ala	Ser	115	120	125	
Gly	Ala	Pro	Arg	Tyr	His	Arg	Val	Ile	His	Ile	Asn	Glu	Val	Val	Leu	130	135	140	
Leu	Asp	Ala	Pro	Val	Gly	Leu	Val	Ala	Arg	Leu	Ala	Asp	Glu	Ser	Gly	145	150	155	160
His	Val	Val	Leu	Arg	Trp	Leu	Pro	Pro	Pro	Glu	Thr	Pro	Met	Thr	Ser	165	170	175	
His	Ile	Arg	Tyr	Glu	Val	Asp	Val	Ser	Ala	Gly	Asn	Gly	Ala	Gly	Ser	180	185	190	
Val	Gln	Arg	Val	Glu	Ile	Leu	Glu	Gly	Arg	Thr	Glu	Cys	Val	Leu	Ser	195	200	205	
Asn	Leu	Arg	Gly	Arg	Thr	Arg	Tyr	Thr	Phe	Ala	Val	Arg	Ala	Arg	Met	210	215	220	
Ala	Glu	Pro	Ser	Phe	Gly	Gly	Phe	Trp	Ser	Ala	Trp	Ser	Glu	Pro	Val	225	230	235	240
Ser	Leu	Leu	Thr	Pro	Ser	Asp	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Gln	Ser	245	250	255	
Lys	Val	Leu	Gly	Val	Phe	Phe	Ala	Glu	Ile	Glu	Gly	Arg	Gly	Thr	Glu	260	265	270	
Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	275	280	285	
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	290	295	300	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	305	310	315	320
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	325	330	335	
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	340	345	350	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	355	360	365	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	370	375	380	

Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	385		390		395		400
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys		405		410		415	
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp		420		425		430	
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys		435		440		445	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser		450		455		460	
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	465		470		475		480
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser		485		490		495	
Leu	Ser	Leu	Ser	Pro	Gly	Lys																
																	500					